OM protein - protein search, using sw model

Run on: March 18, 2004, 08:47:22 ; Search time 0.001 Seconds
                                          (without alignments)
                                          167.310 Million cell updates/sec

GenCore version 5.1.6
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Title: us-09-762-258-2
Perfect score: 2614
Sequence: 1 MARGRRARGAGAAMAAVFDL.........PIRPPSGTKKSKRGRGRPGR 495

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 338 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1 summaries

Database :   us-09-153-939-2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1692	64.7	338	1	us-09-153-939-2

ALIGNMENTS

RESULT 1
us-09-153-939-2

Query Match   64.7%;   Score 1692; DB 1; Length 338;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 315; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   181 EDTACFYLAETTLALGHLHSQGIIYRDLKPENIMLSSQGHIKLTDFGLCKESIHEGAVTH 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   24 EDTACFYLAETTLALGHLHSQGIIYRDLKPENIMLSSQGHIKLTDFGLCKESIHEGAVTH 83

Qy   241 TFCGTIEYMAPEILVRSGHNRAVDWWSLGALMYDMLTGSPPFTAENRKKTMDKIIRGKLA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 TFCGTIEYMAPEILVRSGHNRAVDWWSLGALMYDMLTGSPPFTAENRKKTMDKIIRGKLA 143

Qy   301 LPPYLTPDARDLVKKFLKRNESQRIGGGEPGDAADVQRHPFFRHMNWDDLLAWRVDPFRP 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   144 LPPYLTPDARDLVKKFLKRNESQRIGGGPGDAADVQRHPFFRHMNWDDLLAWRVDPFPRP 203

Qy   361 CLQSEEDVSQPDTRFTRQTPVDSPDDTALSESANQAFLGFTYVAPSVLDSIKEGFSFQPK 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   204 CLQSEEDVSQPDTRFTRQTPVDSPDDTALSESANQAFLGFTYVAPSVLDSIKEGFSFQPK 263

Qy   421 LRSPRRLNSSPRVVSPLKFSPFEGFRPSPSLPEPTELPLPPPLPPPPSTTAPLPIRPP 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   264 LRSPRRLNSSPRVVSPLKFSPFEGFRPSPSLPEPTELPLPPPLPPPPSTTAPLPIRPP 323

Qy   481 SGTKKSKRGRGRPGR 495
          |||||||||||||||
Db   324 SGTKKSKRGRGRPGR 338

Search completed: March 18, 2004, 08:47:22
Job time : 0.001 secs

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OM protein - protein search, using sw model

                          GenCore version 5.1.6
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Run on:          March 18, 2004, 08:47:22 ; Search time 0.001 Seconds
                                             (without alignments)
                                             167.310 Million cell updates/sec

Title:           us-09-762-258-2
Perfect score:   2614
Sequence:        1 MARGRRARGAGAMAAVFDL...........PIRPPSGTKKSKRGRGRPGR 495

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1 seqs, 338 residues

Total number of hits satisfying chosen parameters:        1

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1 summaries

Database :       us-09-153-939-2:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                SUMMARIES

Result             %     Query
No.    Score   Match  Length DB  ID                    Description
-----  -----  ------  ------ --- ---------------       -----------
  1     1692   64.7    338    1  us-09-153-939-2

                                ALIGNMENTS

RESULT 1
us-09-153-939-2

Query Match          64.7%;  Score 1692;  DB 1;  Length 338;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  315; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy   181 EDTACFYLAEITLALGHLHSQGIIYRDLKPENIMLSSQGHIKLTDFGLCKESIHEGAVTH 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    24 EDTACFYLAEITLALGHLHSQGIIYRDLKPENIMLSSQGHIKLTDFGLCKESIHEGAVTH 83

Qy   241 TFCGTIEYMAPEIIVRSGHNRAVDWWSLGALMYDMLTGSPPFTAENRKKTMDKIIRGKLA 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    84 TFCGTIEYMAPEIIVRSGHNRAVDWWSLGALMYDMLTGSPPFTAENRKKTMDKIIRGKLA 143

Qy   301 LPPYLITPDARDLVKKFLKRNPSQRIGGGPGDAADVQRHPFFRHMNWDDLLAWRVDPPRP 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   144 LPPYLITPDARDLVKKFLKRNPSQRIGGGPGDAADVQRHPFFRHMNWDDLLAWRVDPPRP 203

Qy   361 CLQSEEDVSQFDTRFTRQTPVDSPDDTALSESANQAFLGFTYVAPSVLDSIKEGFSFQPK 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   204 CLQSEEDVSQFDTRFTRQTPVDSPDDTALSESANQAFLGFTYVAPSVLDSIKEGFSFQPK 263

Qy   421 LRSPRRLNSSPRVPVSPLKFSPFEGFRPSPLPEPTELPLPPPLPPPPSTTAPLPIRPP 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   264 LRSPRRLNSSPRVPVSPLKFSPFEGFRPSPLPEPTELPLPPPLPPPPSTTAPLPIRPP 323

Qy   481 SGTKKSKRGRGRPGR 495
         |||||||||||||||
Db   324 SGTKKSKRGRGRPGR 338

Search completed: March 18, 2004, 08:47:22
Job time : 0.001 secs
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: March 18, 2004, 08:51:21 ; Search time 1 Seconds
5.982 Million cell updates/sec

Title: us-09-762-258-1
Perfect score: 1816
Sequence: 1 gagagagagagagagaga.........aaaaaaaaaaaaaaaaa 1816

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1647 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-09-153-939-4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
                    %
Result           Query
No.    Score   Match Length  DB    ID                        Description
-----  -----   -----  ------  --    --                        -----------
1     1566.7   86.3   1647    1   us-09-153-939-4
```

ALIGNMENTS

```
RESULT 1
us-09-153-939-4

Query Match     86.3%;  Score 1566.7;  DB 1;  Length 1647;
Best Local Similarity   95.3%;  Pred. No. 0;
Matches 1637; Conservative   0; Mismatches  10;  Indels   71; Gaps   3;

Qy     89 CGACGGGCCCCGGCGGGGGGGGGGGGGGGGGGGGGGG                                    148
          ||||||||||||||||||||||||||
Db      1 CGACGGGCCCCGGCGGGGGGG----CGCCATGGCGGCNNNGTGTTTTGGATTTGGATTTGGAGACG        56

Qy    149 GAGGAAGGCAGCGGAGGGGCGAGGGGCGAGCGCAGAGAGCTCAGCGGCGGACGCACGTGCCCCTT        208
          |||||||||||||||||||||||||||||||||||||||||||
Db     57 GAGGAAGGCAGCGGAGGGGCGAGGGGCGCAGAGCTCAGCGGCGGACGCACGTGCCCCATC        101

Qy    209 GCCGAGTTGAGGGCCAGCTGGCCCTAGAGCCTGTGGGACACTATATGAGAGAGGTGGAGCTGACT        268
          |||||||||||||||||||                      ||||||||||||||||||||
Db    102 ----------------------GCCTGTGGGACACTATTGAAGAGGTGGGAGCTGACT        135

Qy    269 GAGACCACCGTGAAACGTTGCCCCAGAGACGCATGCGGGGGCCCCACTGCTTTTGAGCTGCTGCGT        328
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    136 GAGACCACCGTGAAACGTTGCCCCAGAGACGCCCCAGTACGGGGCCCCACTGCTTTTGAGCTGCTGCGT        195

Qy    329 GTGTGTGGGCCAAGGGGGGGGCTATGGCAAGGTGTGTTGCAAAGGTGCAAGGCACCAC        388
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    196 GTGCTGGGCCAAGGGGGGCCTATGGCGCAAGGTGTTCAGGTGCGAAAGGTGCAAGGCACCAAC        255

Qy    389 TTGGGCAAAATATATGCCATTGAAAAGTCCTTAAGGAAGCCCAAAAAATTGTCGCGAATGCCAAG        448
          |||||||||||
Db    256 TTGGGCAAAATATATGCCATTGAAAAGTCCTTAAGGAAGCCCAAAAAATTGTCGCGAATGCCAAG        315

Qy    449 GACACAGCACACACACGGGCTGAGCGGAACAATTCTAGAGTCAGTGAAAGTCAGTGAAGTACGGCC        508
          |||||||||||||||||||||||||||||||||||||||||
Db    316 GACACAGGCACACACACGGGCTGAGCGGAACAATTCTAGAGTCAGTGAAGTCAGTGAAGGACCCTTTATT        375

Qy    509 GTGGAAACTGGCCTATGCCTTCAGACTGTGTGGGGCAAAACTCACCTCGTCCATCCTTGAGTCTC        568
          ||||||||||||||||||||||||||||||||
Db    376 GTGGAACTGGGCCTATGCCTTCAGACTGGTGGGGCAAAACTCTACCTCGTCCTTGAGTGCCTC        435

Qy    569 AGTGGGTGGGCGAGCTCTTCACGCATCTGGAGCGAGGAGGGGCCATCTTCCTGGAAGATACGGCC        628
          ||||||||                                ||||||||||||||
Db    436 AGTGGGTGGGCAGCTCTTCTG---------GAAGATACGGGC        469

Qy    629 TGCTTCTACCTTGGCTGAGCTGAGATCACGGCTGGCCCTGGGCCCATCTCCACTCCCAGGGCATCATC        688
          ||||||||||||||||||||||||||||||||||||||
Db    470 TGCTTCTACCTTGGCTGAGATCACGGCTGGCCCTGGGCCCATCTCCACTCCCAGGGCATCATC        529

Qy    689 TACCGGGACCTCAACCCCCAGAACATCACTCCTCAGCAGCGCAGGGCCACAACTGACCACGAACC        748
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    530 TACCGGGACCTCAAGCCCGAGAACATCATGCTCAGCAGCGCCAGGGCCACAATCAAAACTGACC        589

Qy    749 GACCTTTGACCTCGAAGGAGTCTATCCATCGAAGGGCGCGGCGCGCACTCACACCTTCTCTGGGGC        808
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    590 GACCTTTGACCTCGAAGGAGTCAATCCATGAGAGGGGCGCGTCACTCACACTTCTGTGGGGC        649

Qy    869 TGGTGGGACGTGGGGGGCCCTGATGTACGACACATGCTTCACTGGATCCCGCGCCCTTTACGGCA        928
          |||||||||||||||||||||||||||||||||||||||||||||
Db    650 ACCATTGAGTACATGGGCCCTGAGATTCGTGGTGGGCAGTGGCCATGGCCACAACCGGGCTGTGGAC        709

Qy    809 ACCATTGAGTACATGGGGCCCTGAGATTCGTGGTGGGCCGTGGCCAGGGCCACAACCGGGGCTGTGGAC        868

Qy    929 CTCACCCCAGATGCCCGGGGACCTTGTCAAACCATGGCAACATCCAGCCAGCCAGTGG        988
          |||||||||||||||||||||||||||||||||||||||||
Db    770 GAGAACCGGGAAGAAAACCATGAATAAGATCATCAGGGGCGAAGCTGGCCACTGGCCCCCCTAC        829

Qy    710 TGGTGGGACGTGGGGGGCCCTGATGTACGACACATGCTTCACTGGATCCCGCGCCCTTTACGGCA        769

Qy    989 GAGAACCGGGAAGAGAAAAACCATGGATAAGATCATCAGGGGCGAAGCTGGCCAGTGGCCACTGGCCCCCCTAC        1048
          ||||||||||||||||||||||||||||||||
Db    830 CTCACCCCAGATGCCCGGGGACCTTGTCAAAACCATGGCAACATCCAGCCCAGCCAGCCAGTGG        889

Qy   1049 ATTGGGGGGGTGGCCCCAGGGGATGCTGCTTGGTGTTGTGATGTGAGAGACACATCCCTTTTTTCCGGCACACATG        1108
          ||||||||||||||||||||||||||||||||
Db    890 ATTGGGGGGGTGGCCCCAGGGGATGCTGCTTGGTGTTGTGATGTGAGAGACACATCCCTTTTTTCCGGCACACATG        949

Qy   1109 AATTGGACGACGACTTCTCTGCCCTGGCCGTGTGGGACCCCCCTTTTCAGCGCCCGTCTGCAGTCA        1168
          ||||||||||||||||||||||||||||||||||||||||||
Db    950 AATTGGACGACCTTCTCTGCCCTGGCCGTGTGGGACCCCCCTTTTCAGCGCCCGTCTGCAGTCA        1009

Qy   1169 GAGGAGGACGTGAGCCAGTTTGATACCCGCGTTCACACGGCAGACGCGGGTGACAGTCCT        1228
          |||||||||||||||||||||||||||||||||||||||||
Db   1010 GAGGAGGACGTGAGCCAGTTTGATACCCGCGTTCACACGGGCAGACGCGGGTGACAGTCCT        1069

Qy   1229 GATGACACAGCCCTCAGCGAGAGTGCCAACCAGGCCTTCACACGGTGCG        1288
          ||||||||||||||||||||||||||||||||||||||
Db   1070 GATGACACAGCCCTCAGCGAGAGTGCCAACCAGGCCTTCAGCGGTTCACACACGTGGGG        1129

Qy   1289 CCGTCTGCCTGGACTGCAGCATCAAGGGAGGGCTTCTCCTTCCAGCCCAAGGTGCGTCACCC        1348
          ||||||||||||||||||||||||||||||||||||
Db   1130 CCGTCTGCCTGGACTGCAGCATCAAGGAGGGCTTCTCCTTCCAGCCCAAGGTGCGTCACCC        1189

Qy   1349 AGGGGCCTCAACGTAGCCCCCGGGGTCCCGCCCTCAGCCCTCAAGTTCTCCCCCTTGAG        1408
          ||||||||||||||||||||||||||||||||||||
Db   1190 AGGCGCCCTCAACGTAGCCCCCGGGTCCCGCCCTCAGCCCTCAAGTTCTCCCCCTTGAG        1249

Qy   1409 GGGGTTTCGGCCCAGAGCCCAGCGCCGGAGGCGCACGGAGGAGCTACCTTCACTTACCTCCTG        1468
          ||||||||||||||||||||||||||||||||||||
Db   1250 GGGTTTCGGCCCAGCGCCCAGCGCCCGGAGGCGCACGGAGGAGCTACCTTCACTTACCTCCTG        1309

Qy   1469 CCACCGCGCGCCCCTCGACCACCGCCCTTCCCCCATCGTCCCGGTCTAGGGAAGGGGACCACTCCTG        1528
          ||||||||||||||||||||||||||||||||||||
Db   1469 CCACCGCGCGCCCCTCGACCACCGCCCTTCCCCCATCGTCCCGGTCTAGGGAAGGGGACCACTCCTG        1528
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Db   1310  CCACCGCGCGCCGCCCCTCGACCACCGACCCCTTCTCCCATCCGTCCCCCCTTCAGGGACCAAG  1369
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1529  AAGTCCAAGAGAGGGGCCCGTGGGGCGTCCAGGGCGTTAGGAAAGCCGGGTGGGGGTGAGGGTAG  1588
                 ||||||||||||  ||||||  ||||  ||  ||||||  ||||||||||||||||||||||||||
Db   1370  AAGTCCAAGAGAGGGGGCCGTGGGGCGTCCAGGGCCGCTAGGAAAGCCGGGGTGGGGGGTAG     1429

Qy   1589  CCCCTTGAGCCCTGTCCCTGCCGGCTGTGAGAGCAGCAGGACCCCTGGGCCCAGTTCCAGAGAC   1648
                 ||  ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db   1430  CCCTTTGAGCCCTGTCCCCGCCGGCTGTGAGAGCAGCAGGACCCCTGGGCCCAGTTCCAGAGAC   1489

Qy   1649  CTGGGGGGTGGTGTTCTTGGGGGGTGGGGTGTGAGTGGGTATTGAAAAGTGTGTGTTCTGGGGGCA  1708
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1490  CTGGGGGGTGTGTCTGGGGGGTGGGGGTTGTGAGTGCCTATGAAAAGTGTGTGTTCTCTGGGGCA   1549

Qy   1709  GCTGTGCCCCTGAATCATGGGCACGGAGGGCCGCCCACCCCGCCGGCTCAACTGCTC         1768
                 ||||||||||||||||  |||||||||||||||||||||||||||||||  ||||||
Db   1550  GCTGTGCCCCTGAATCATGGGCACGGAGGGCCGCCCCACCCCGGCTCAACTGCTG          1609

Qy   1769  CCGTGGAAGATTAAAGGGCTGAATCATGAAAAAAAAA   1806
                 ||||||||||||||||||||||||||||||||||
Db   1610  CCGTGGAAGATTAAAGGGCTGAATCATGAAAAAAAAAA   1647
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Search completed: March 18, 2004, 08:51:23
Job time : 2 secs